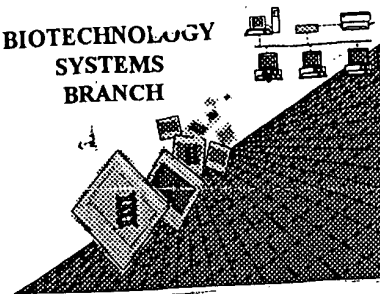


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/977,137

Source: OIPE

Date Processed by STIC: 11/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/977,137

DATE: 11/01/2001

TIME: 08:32:44

Input Set : A:\ES.txt

Output Set: N:\CRF3\11012001\I977137.raw

Does Not Comply
Corrected Diskette Needed

OK> 3 <110> APPLICANT: Summers, Anne O.
 4 Caguiat, Jonathan
 6 <120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
 7 Methods
 9 <130> FILE REFERENCE: 79-00
 11 <140> CURRENT APPLICATION NUMBER: US/09/977,137
 12 <141> CURRENT FILING DATE: 2001-10-12
 14 <150> PRIOR APPLICATION NUMBER: US 60/240,465
 15 <151> PRIOR FILING DATE: 2000-10-12
 17 <160> NUMBER OF SEQ ID NOS: 18 (see pp 3-5)
 19 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

89 <210> SEQ ID NO: 4
 90 <211> LENGTH: 117
 91 <212> TYPE: PRT
 92 <213> ORGANISM: Artificial Sequence
 94 <220> FEATURE:
 95 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
 97 <400> SEQUENCE: 4
 98 Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys
 99 1 5 10 15
 101 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
 102 20 25 30
 104 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
 105 35 40 45
 107 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
 108 50 55 60
 110 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
 111 65 70 75 80
 113 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
 114 85 90 95
 116 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
 117 100 105 110
 E--> 119 Pro Gln Phe Glu Lys 115 (insert)
 W--> 121 <110> APPLICANT: Summers, Anne O.
 W--> 121 <110> APPLICANT: Summers, Anne O.
 W--> 124 <120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
 W--> 124 <120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
 W--> 125 Methods
 W--> 127 <130> FILE REFERENCE: 79-00
 W--> 127 <130> FILE REFERENCE: 79-00
 W--> 129 <140> CURRENT APPLICATION NUMBER: unassigned
 130 <141> CURRENT FILING DATE: 2001-10-12
 W--> 132 <150> PRIOR APPLICATION NUMBER: US 60/240,465

SEQUENCE LISTING

What is this
 ? delete

see next page

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/977,137DATE: 11/01/2001
TIME: 08:32:44

Input Set : A:\ES.txt

Output Set: N:\CRF3\11012001\I977137.raw

W--> 133 <151> PRIOR FILING DATE: 2000-10-12
W--> 135 <160> NUMBER OF SEQ ID NOS: 18
W--> 135 <160> NUMBER OF SEQ ID NOS: 18
W--> 137 <170> SOFTWARE: PatentIn Ver. 2.0

delete

207 <210> SEQ ID NO: 4

208 <211> LENGTH: 117

209 <212> TYPE: PRT

210 <213> ORGANISM: Artificial Sequence

212 <220> FEATURE:

213 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon

215 <400> SEQUENCE: 4

216 Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys

217 1 5 10 15

219 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu

220 20 25 30

222 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys

223 35 40 45

225 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu

226 50 55 60

228 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met

229 65 70 75 80

231 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala

232 85 90 95

234 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His

235 100 105 110

237 Pro Gln Phe Glu Lys Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu

238 50 55 60

E--> 238 50 55 60

240 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Gln Met

241 65 70 75 80

E--> 241 65 70 75 80

243 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala

244 85 90 95

E--> 244 85 90 95

246 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His

247 100 105 110

E--> 247 100 105 110

249 Pro Gln Phe Glu Lys

E--> 250 115

E--> 253 <210> SEQ ID NO: 9

ignore - see pp 3-5

<170> PatentIn Ver. 2.0

<210> 1

<211> 435

<212> DNA

<213> Shigella flexneri, Tn21 of Plasmid R100

The following duplicate text appears after the duplicate

<170>, as shown on P. 2

<400> 1
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ggcagcatcc gccgctatgg ggaggcggac gtggttcggg tgaaattcgt gaaatcggca 180
cagcggtctg ggttcagtct ggacgagatt gccgagctgt tgcggctcga cgatggcacc 240
cactgcgagg aggccagcag cctggccgaa cacaagctca aggacgtgcg cgagaagatg 300
gccgacttgg cgcgcatgga aaccgtgctg tctgaactcg tgtgcgcctg ccatgcacga 360
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<211> 144

<212> PRT

<213> Shigella flexneri, Tn21 of Plasmid R100

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Met Glu Asn Asn Leu Glu Asn Leu Thr Ile Gly Val Phe Ala Lys Ala
1 5 10 15
Ala Gly Val Asn Val Glu Thr Ile Arg Phe Tyr Gln Arg Lys Gly Leu
20 25 30
Leu Arg Glu Pro Asp Lys Pro Tyr Gly Ser Ile Arg Arg Tyr Gly Glu
35 40 45
Ala Asp Val Val Arg Val Lys Phe Val Lys Ser Ala Gln Arg Leu Gly
50 55 60
Phe Ser Leu Asp Glu Ile Ala Glu Leu Leu Arg Leu Asp Asp Gly Thr
65 70 75 80
His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val
85 90 95
Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu
100 105 110
Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Leu
115 120 125
Ile Ala Ser Leu Gln Gly Glu Ala Gly Leu Ala Arg Ser Ala Met Pro
130 135 140

duplicate

<210> 3

<211> 321

<212> DNA

duplicate

<213> Artificial Sequence

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<223> Description of Artificial Sequence: chelon

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 aagatggccg acttggcgcg catggaaacc gtgctgtctg aactcgtgtg cgctgccat 120
 gcacgaaagg ggaatgtttc ctgcccgttg atcgcgtcac tacagggatc ctcaggcacc 180
 cactgcgagg aggccagcag cctggccgaa cacaagctca aggacgtgcg cgagaagatg 240
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<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chelon

<400> 4
 Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys
 1 5 10 15

Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
 20 25 30

Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
 35 40 45

Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
 50 55 60

Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
 65 70 75 80

Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
 85 90 95

Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
 100 105 110

Pro Gln Phe Glu Lys 55 Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
 50 60

Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Gln Met
 65 70 75 80

Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
 85 90 95

Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
 100 105 110

Pro Gln Phe Glu Lys
 115

duplicate

duplicate

09/977,137 5

Then, jump to Sequence 9
(Sequence 5 through 8
missing)

<210> 9

RMF

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/977,137

DATE: 11/01/2001
TIME: 08:32:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\11012001\I977137.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:119 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:119 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:119 M:252 E: No. of Seq. differs, <211>LENGTH:Input:117 Found:119 SEQ:4
L:121 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:121 M:281 W: Numeric Fields not Ordered, <110> not ordered!
L:124 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:124 M:281 W: Numeric Fields not Ordered, <120> not ordered!
L:127 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:127 M:281 W: Numeric Fields not Ordered, <130> not ordered!
L:129 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:129 M:281 W: Numeric Fields not Ordered, <140> not ordered!
L:129 M:270 C: Current Application Number differs, Replaced Current Application Number
L:130 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:130 M:281 W: Numeric Fields not Ordered, <141> not ordered!
L:132 M:281 W: Numeric Fields not Ordered, <150> not ordered!
L:133 M:281 W: Numeric Fields not Ordered, <151> not ordered!
L:135 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:135 M:281 W: Numeric Fields not Ordered, <160> not ordered!
L:137 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:238 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:250 M:252 E: No. of Seq. differs, <211>LENGTH:Input:117 Found:181 SEQ:4
L:253 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 5 thru 8

11/1/01